Amendments to the Specification:

Please delete current Abstract at page 38 and insert new Abstract as attached.

Please replace the paragraph beginning at page 3, line 4 with the following amended paragraph:

In certain embodiments of the invention, mutations can be introduced into one or both nucleic acids to promote allele-specific four-way complex migration. Such mutations are typically near the site of a polymorphism and do not impede four-way complex migration unless the nucleic acids differ at the site of the polymorphism. Such mutations are described in detail in copending U.S. application no. 10/071,302 ~~(attorney docket no. 10752-016-999),~~ the contents of which are hereby incorporated by reference in their entirety.

Please replace the paragraph beginning at page 4, line 13 with the following amended paragraph:

~~FIG. 1 provides~~ FIG. 1A and FIG. 1B provide an illustration of the preparation of a typical partial duplex of nucleic acid by PCR and formation of four-way complexes **C1**, **C2**, **C3**, and **C4**, which are then subject to branch migration conditions; FIG. 1A illustrates that if there is no mismatch between sequences **A** and **B**, each of the four complexes **C1**, **C2**, **C3**, and **C4** resolves into duplexes; and FIG. 1B illustrates that if there is a mismatch or mismatches between sequences **A** and **B**, each of the four complexes **C1**, **C2**, **C3**, and **C4** forms a stabilized four-way complex;

Please replace the paragraph beginning at page 15, line 15, with the following amended paragraph:

In a preferred embodiment of the invention, the nucleic acids can be prepared to detect a single base mutation between the target nucleic acid and the reference nucleic acid according to the methods described in co-pending U.S. application no 10/071,302 ~~(attorney docket no. 10752-016-999)~~, the content of which is hereby incorporated by reference in its entirety. Briefly, in order to increase the sensitivity of the present detection method for a single base difference between short (<100 bp) target and reference nucleic acids, an additional mutation can be introduced either 5' or 3' to the site of the potential difference in either the target nucleic acid or

in the reference nucleic acid. The additional mutation can be introduced, for instance, by using a forward primer that hybridizes to a sequence 5' of the potential single base difference and is capable of introducing such a mutation. Or alternatively, the additional mutations can be introduced by using a reverse primer that hybridizes to a sequence 3' of the potential single base difference and is capable of introducing such a mutation. Other methods of introducing such mutations will be apparent to those of skill in the art. For instance, the mutation can be introduced in two synthetic oligos that correspond to each of the two strands of reference partial duplexes and therefore can be used to make the desired reference partial duplexes with predefined mutations.

Please replace the paragraph beginning at page 28, line13 with the following amended paragraph:

Five regions of human genomic DNA that contain known single-nucleotide polymorphisms (SNPs) were PCR-amplified using tailed reverse primers to enable the formation of four-way complexes. The sequence of these regions, the location and identity of the respective SNPs within them and the sequences of the primers can be found in the National Center for Biotechnology Information (NCBI) SNP database (NCBI). A database of single nucleotide polymorphisms shown at the web site of www.ncbi.nlm.nih.gov/SNP. ~~http://www.ncbi.nlm.nih.gov/SNP/index.html).~~ The NCBI ~~assay ID's~~ accession IDs of the SNPs used were as follows: ss4215, ss4217, ss4213, ss4141, ss4212 and ss4030.